

IN THE CLAIMS:

1. (currently amended) A method of using a mutation scanning array, wherein said mutation scanning array comprises a plurality of elements, wherein the elements contain immobilized oligonucleotides 8 - 50 bases long, that collectively span at least 10 different ~~whole~~ genes from the 5' to 3' end, wherein the genes can be either coding regions or the genomic genes, to identify mutations in a target DNA sequence which comprises:
  - (a) hybridizing the target DNA with a control DNA sequence to create a duplex, wherein the control DNA sequence is the wild-type DNA corresponding to the target DNA sequence,
  - (b) tagging any mismatch in said duplex with a detectable moiety,
  - (c) cleaving the duplex into segments of 50 - 300 bases,
  - (d) removing the segments tagged with the detectable moiety,
  - (e) contacting the segments tagged with the detectable moiety with the mutation scanning array, and
  - (f) identifying in which gene and gene segment the selected mismatch belongs to.
2. (currently amended) The method of claim 1 ~~claim 10~~, wherein the segments tagged with the detectable moiety are amplified before being used on the mutation scanning array.
3. (original) The method of claim 1 or 2, wherein the whole gene is represented by array elements; each element containing immobilized oligonucleotides that sample in 25-300 bases for the whole 3' to 5' mRNA sequence of each represented gene.
4. (currently amended) The method of claim 1 or 2, wherein each of the ~~whole~~ genes is represented by the coding ~~genomic~~ portion of the gene.

5. (currently amended) The method of claim 1 or 2, wherein each of the ~~whole~~ genes is represented by both the coding and non-coding genomic portions of a gene.
6. (currently amended) The method of claim 1 or 2, wherein said at least 10 different genes are ~~selected from the genome~~, collectively known to predispose an individual to a particular disease.
7. (original) The method of claim 6, where the disease is a particular kind of cancer.
8. (original) The method of claim 6, where the disease is a cardiovascular abnormality, or a neurodegenerative disorder, or diabetes.
9. (currently amended) The method of claim 1 or 2, where said ~~the~~ genes ~~selected~~ are all known tumor suppressor genes or oncogenes.
10. (currently amended) The method of claim 1 or 2, where said ~~the~~ genes ~~selected~~ are genes known to be overexpressed in a malignant cell, wherein overexpression is determined by comparison to the gene's expression in a corresponding non-malignant cell.
11. (original) The method of claim 1, wherein the array is a chip or a microsphere.
12. (original) A method of using a mutation scanning array to identify mutation in a large DNA sequence, wherein said mutation scanning array comprises a plurality of elements, wherein the elements contain immobilized oligonucleotides 8 - 50 bases long, that collectively span at least 5 different genes, wherein said method comprises:
  - (a) hybridizing the target DNA sequence with a control DNA sequence wherein said control DNA sequence is the wild-type DNA sequence corresponding to the target DNA sequence to create a duplex;
  - (b) digesting the duplex to fragments of 50-300 base pairs, with restriction enzymes that allow generic addition of PCR primers;

- (c) adding PCR primers to the duplex
  - (d) treating the duplex to remove any spontaneous aldehydes;
  - (e) reacting the duplex with a repair glycosylase to convert any mismatched sites in the duplex to reactive sites containing an aldehyde-containing abasic site;
  - (f) reacting the duplex with a compound of the formula X-Z-Y, wherein X is a detectable moiety, Y is NHNH<sub>2</sub>, O-NH<sub>2</sub> or NH<sub>2</sub>, and Z is a hydrocarbon, alkyhydroxy, alkylethoxy, alkylester, alkylether, alkylamide or alkylamine, wherein Z may be substituted or unsubstituted; or where Z may contain a cleavable group; for a sufficient time and under conditions to covalently bind to the reactive sites;
  - (g) detecting the bound compound to identify sites of mismatches;
  - (h) isolating the DNA that contains mismatches from DNA without mismatches;
  - (i) PCR-amplifying the mismatch-containing DNA
  - (j) applying the mismatch-containing DNA on the Mutation Scanning Array, to determine the genomic position(s) where mismatches occur; and
  - k) determining whether the mismatch is a mutation or polymorphism.
13. (original) The method of claim 12, where the detectable moiety is selected from the group consisting of NH<sub>2</sub>, SH, NHNH<sub>2</sub>, a fluorescein derivative, a hydroxycoumarin derivative, a rhodamine derivative, a BODIPY derivative, a digoxigenin derivative and a biotin derivative.
14. (withdrawn)
15. (withdrawn)